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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/895,263B

DATE: 12/06/2003

TIME: 10:47:55

Input Set : A:\PTO.YF.txt

Output Set: N:\CRF4\12062003\I895263B.raw

3 <110> APPLICANT: He, et al.  
 5 <120> TITLE OF INVENTION: Antibodies to Interleukin-1 Beta Converting Enzyme Like Apoptosis

6 Protease 3  
 7 and 4

9 &lt;130&gt; FILE REFERENCE: PF140C2

11 &lt;140&gt; CURRENT APPLICATION NUMBER: 09/895,263B

12 &lt;141&gt; CURRENT FILING DATE: 2001-07-02

14 &lt;150&gt; PRIOR APPLICATION NUMBER: 08/334,251

15 &lt;151&gt; PRIOR FILING DATE: 1994-11-01

17 &lt;160&gt; NUMBER OF SEQ ID NOS: 14

19 &lt;170&gt; SOFTWARE: PatentIn version 3.2

21 &lt;210&gt; SEQ ID NO: 1

22 &lt;211&gt; LENGTH: 1369

23 &lt;212&gt; TYPE: DNA

24 &lt;213&gt; ORGANISM: Homo sapiens

26 &lt;400&gt; SEQUENCE: 1

27	gcacgagaaa	ctttgctgtg	cgcgttctcc	cgcgcgcggg	ctcaactttg	tagagcgagg	60
29	ggccaacttg	gcagagcgcg	cggccagctt	tgcagagagc	gccctccagg	gactatgcgt	120
31	gcggggacac	gggtcgcttt	gggtctctcc	acccctgcgg	agcgcactac	cccagaccag	180
33	gggcggtgca	agccccgccc	ggccctaccc	agggcggtct	ctccctccgc	agcgccgaga	240
35	cttttagttt	cgctttcgct	aaaggggccc	cagacccttg	ctgcggagcg	acggagagag	300
37	actgtgccag	tcccagccgc	cctaccgcgc	tgggaacgat	ggcagatgat	cagggctgta	360
39	ttgaagagca	gggggttgag	gattcagcaa	atgaagattc	agtggatgct	aagccagacc	420
41	ggtcctcggt	tgtaccgtcc	ctcttcagta	agaagaagaa	aaatgtcacc	atgcgatcca	480
43	tcaagaccac	ccgggaccga	gtgcctacat	atcagtacaa	catgaatttt	gaaaagctgg	540
45	gcaaattgcat	cataataaac	aacaagaact	ttgataaagt	gacaggtatg	ggcgttcgaa	600
47	acggaacaga	caaagatgcc	gagggcgctct	tcaagtgctt	ccgaagcctg	ggttttgacg	660
49	tgattgtcta	taatgactgc	tcttggtgcca	agatgcaaga	tctgcttaaa	aaagcttctg	720
51	aagaggacca	tacaaatgcc	gcctgcttcg	cctgcatcct	cttaagccat	ggagaagaaa	780
53	atgtaattta	tgggaaagat	ggtgtcacac	caataaagga	tttgacagcc	cactttaggg	840
55	gggatagatg	caaaaccctt	ttagagaaac	ccaaactctt	cttcattcag	gcttgccgag	900
57	ggaccgagct	tgatgatgcc	atccaggccg	actcggggcc	catcaatgac	acagatgcta	960
59	atcctcgata	caagatccca	gtggaagctg	acttctctct	cgcctattcc	acggttccag	1020
61	gctattactc	gtggaggagc	ccaggaagag	gctcctgggt	tgtgcaagcc	ctctgctcca	1080
63	tcctggagga	gcacggaaaa	gaccttgaaa	tcattgcagat	cctcaccagg	gtgaatgaca	1140
65	gagttgccag	gcactttgag	tctcagtcgt	atgaccacaa	cttccatgag	aagaagcaga	1200
67	tcccctgtgt	gggtctccatg	ctcaccaagg	aactctactt	cagtcaatag	ccatatcagg	1260
69	ggtacattct	agctgagaag	caatgggtca	ctcattaatg	aatcacattt	ttttatgctc	1320
71	ttgaaatatt	cagaaattct	ccaggatttt	aatttcagga	aaatgtatt		1369

74 &lt;210&gt; SEQ ID NO: 2

75 &lt;211&gt; LENGTH: 303

76 &lt;212&gt; TYPE: PRT

77 &lt;213&gt; ORGANISM: Homo sapiens

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79 &lt;400&gt; SEQUENCE: 2

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81 Met Ala Asp Asp Gln Gly Cys Ile Glu Glu Gln Gly Val Glu Asp Ser
82 1          5          10          15
85 Ala Asn Glu Asp Ser Val Asp Ala Lys Pro Asp Arg Ser Ser Phe Val
86          20          25          30
89 Pro Ser Leu Phe Ser Lys Lys Lys Asn Val Thr Met Arg Ser Ile
90          35          40          45
93 Lys Thr Thr Arg Asp Arg Val Pro Thr Tyr Gln Tyr Asn Met Asn Phe
94          50          55          60
97 Glu Lys Leu Gly Lys Cys Ile Ile Ile Asn Asn Lys Asn Phe Asp Lys
98 65          70          75          80
101 Val Thr Gly Met Gly Val Arg Asn Gly Thr Asp Lys Asp Ala Glu Ala
102          85          90          95
105 Leu Phe Lys Cys Phe Arg Ser Leu Gly Phe Asp Val Ile Val Tyr Asn
106          100          105          110
109 Asp Cys Ser Cys Ala Lys Met Gln Asp Leu Leu Lys Lys Ala Ser Glu
110          115          120          125
113 Glu Asp His Thr Asn Ala Ala Cys Phe Ala Cys Ile Leu Leu Ser His
114          130          135          140
117 Gly Glu Glu Asn Val Ile Tyr Gly Lys Asp Gly Val Thr Pro Ile Lys
118 145          150          155          160
121 Asp Leu Thr Ala His Phe Arg Gly Asp Arg Cys Lys Thr Leu Leu Glu
122          165          170          175
125 Lys Pro Lys Leu Phe Phe Ile Gln Ala Cys Arg Gly Thr Glu Leu Asp
126          180          185          190
129 Asp Ala Ile Gln Ala Asp Ser Gly Pro Ile Asn Asp Thr Asp Ala Asn
130          195          200          205
133 Pro Arg Tyr Lys Ile Pro Val Glu Ala Asp Phe Leu Phe Ala Tyr Ser
134          210          215          220
137 Thr Val Pro Gly Tyr Tyr Ser Trp Arg Ser Pro Gly Arg Gly Ser Trp
138 225          230          235          240
141 Phe Val Gln Ala Leu Cys Ser Ile Leu Glu Glu His Gly Lys Asp Leu
142          245          250          255
145 Glu Ile Met Gln Ile Leu Thr Arg Val Asn Asp Arg Val Ala Arg His
146          260          265          270
149 Phe Glu Ser Gln Ser Asp Asp Pro His Phe His Glu Lys Lys Gln Ile
150          275          280          285
153 Pro Cys Val Val Ser Met Leu Thr Lys Glu Leu Tyr Phe Ser Gln
154          290          295          300

```

157 &lt;210&gt; SEQ ID NO: 3

158 &lt;211&gt; LENGTH: 1159

159 &lt;212&gt; TYPE: DNA

160 &lt;213&gt; ORGANISM: Homo sapiens

162 &lt;400&gt; SEQUENCE: 3

```

163 gcacgagcgg atgggtgcta ttgtgaggcg gttgtagaag agtttcgtga gtgctcgcag      60
165 ctcatacctg tggtgtgta tccgtggcca cagctggttg gcgtgcctt gaaatcccag      120
167 gccgtgagga gttagcgagc cctgctcaca ctgcgcgtc tggttttcgg tgggtgtgcc      180
169 ctgcacctgc ctcttcccgc attctcatta ataaaggtat ccatggagaa cactgaaaac      240
171 tcagtggatt caaatccat taaaaatttg gaaccaaaga tcatacatgg aagcgaatca      300

```

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173 atggactctg gaatatccct ggacaacagt tataaaatgg attatcctga gatgggttta 360
175 tgtataataa ttaataataa gaattttcat aaaagcactg gaatgacatc tcggtctggt 420
177 acagatgtcg atgcagcaaa cctcagggaa acattcagaa acttgaaata tgaagtcagg 480
179 aataaaaaatg atcttacacg tgaagaaatt gtggaattga tgcgtgatgt ttctaaagaa 540
181 gatcacagca aaaggagcag ttttgtttgt gtgcttctga gccatggtga agaaggaata 600
183 attttttgaa caaatggacc tgttgacctg aaaaaaataa caaacttttt cagaggggat 660
185 cgttgtagaa gtctaactgg aaaacccaaa cttttcatta ttcaggcctg ccgtggtaca 720
187 gaactggact gtggcattga gacagacagt ggtgttgatg atgacatggc gtgtcataaa 780
189 ataccagtgg aggccgactt cttgtatgca tactccacag cacctggtta ttattcttgg 840
191 cgaaattcaa aggatggctc ctggttcac cagtcgcttt gtgccatgct gaaacagtat 900
193 gccgacaagc ttgaatttat gcacattctt acccggttta accgaaaggt ggcaacagaa 960
195 tttgagtcct tttcctttga cgctactttt catgcaaaga aacagattcc atgtattggt 1020
197 tccatgctca caaaagaact ctatttttat cactaaagaa atggttggtt ggtggttttt 1080
199 tttagtttgt atgccaagtg agaagatggt atatttgggt actgtatttc cctctcattg 1140
201 gggacctact ctcatgctg 1159
204 <210> SEQ ID NO: 4
205 <211> LENGTH: 277
206 <212> TYPE: PRT
207 <213> ORGANISM: Homo sapiens
209 <400> SEQUENCE: 4
211 Met Glu Asn Thr Glu Asn Ser Val Asp Ser Lys Ser Ile Lys Asn Leu
212 1 5 10 15
215 Glu Pro Lys Ile Ile His Gly Ser Glu Ser Met Asp Ser Gly Ile Ser
216 20 25 30
219 Leu Asp Asn Ser Tyr Lys Met Asp Tyr Pro Glu Met Gly Leu Cys Ile
220 35 40 45
223 Ile Ile Asn Asn Lys Asn Phe His Lys Ser Thr Gly Met Thr Ser Arg
224 50 55 60
227 Ser Gly Thr Asp Val Asp Ala Ala Asn Leu Arg Glu Thr Phe Arg Asn
228 65 70 75 80
231 Leu Lys Tyr Glu Val Arg Asn Lys Asn Asp Leu Thr Arg Glu Glu Ile
232 85 90 95
235 Val Glu Leu Met Arg Asp Val Ser Lys Glu Asp His Ser Lys Arg Ser
236 100 105 110
239 Ser Phe Val Cys Val Leu Leu Ser His Gly Glu Glu Gly Ile Ile Phe
240 115 120 125
243 Gly Thr Asn Gly Pro Val Asp Leu Lys Lys Ile Thr Asn Phe Phe Arg
244 130 135 140
247 Gly Asp Arg Cys Arg Ser Leu Thr Gly Lys Pro Lys Leu Phe Ile Ile
248 145 150 155 160
251 Gln Ala Cys Arg Gly Thr Glu Leu Asp Cys Gly Ile Glu Thr Asp Ser
252 165 170 175
255 Gly Val Asp Asp Asp Met Ala Cys His Lys Ile Pro Val Glu Ala Asp
256 180 185 190
259 Phe Leu Tyr Ala Tyr Ser Thr Ala Pro Gly Tyr Tyr Ser Trp Arg Asn
260 195 200 205
263 Ser Lys Asp Gly Ser Trp Phe Ile Gln Ser Leu Cys Ala Met Leu Lys
264 210 215 220
267 Gln Tyr Ala Asp Lys Leu Glu Phe Met His Ile Leu Thr Arg Val Asn

```

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```

268 225          230          235          240
271 Arg Lys Val Ala Thr Glu Phe Glu Ser Phe Ser Phe Asp Ala Thr Phe
272          245          250          255
275 His Ala Lys Lys Gln Ile Pro Cys Ile Val Ser Met Leu Thr Lys Glu
276          260          265          270
279 Leu Tyr Phe Tyr His
280          275
283 <210> SEQ ID NO: 5
284 <211> LENGTH: 31
285 <212> TYPE: DNA
286 <213> ORGANISM: Artificial sequence
288 <220> FEATURE:
289 <223> OTHER INFORMATION: Contains a Bam HI restriction enzyme site (underlined)
followed
290      by 18 nucleotides of ICE-LAP-3 coding sequence starting from the
291      presumed terminal amino acid of the processed protein codon
293 <400> SEQUENCE: 5
294 gatcggatcc atgcgtgcgg ggacacgggt c 31
297 <210> SEQ ID NO: 6
298 <211> LENGTH: 31
299 <212> TYPE: DNA
300 <213> ORGANISM: Artificial sequence
302 <220> FEATURE:
303 <223> OTHER INFORMATION: Contains complementary sequences to an Xba I site followed
by 21
304      nucleotides of ICE-LAP-3
306 <400> SEQUENCE: 6
307 gtactctaga tcattcaccc tgggtggagga t 31
310 <210> SEQ ID NO: 7
311 <211> LENGTH: 31
312 <212> TYPE: DNA
313 <213> ORGANISM: Artificial sequence
315 <220> FEATURE:
316 <223> OTHER INFORMATION: Contains a Bam HI restriction enzyme site followed by 18
317      nucleotides of ICE-LAP-4 coding sequence starting from the
318      presumed terminal amino acid of the processed protein codon
320 <400> SEQUENCE: 7
321 gatcggatcc atggagaaca ctgaaaactc a 31
324 <210> SEQ ID NO: 8
325 <211> LENGTH: 31
326 <212> TYPE: DNA
327 <213> ORGANISM: Artificial sequence
329 <220> FEATURE:
330 <223> OTHER INFORMATION: Contains complementary sequences to an Xba I site followed
by 21
331      nucleotides of ICE-LAP-4
333 <400> SEQUENCE: 8
334 gtactctaga ttagtgataa aaatagagtt c 31
337 <210> SEQ ID NO: 9
338 <211> LENGTH: 22
339 <212> TYPE: DNA
340 <213> ORGANISM: Artificial sequence

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342 <220> FEATURE:
343 <223> OTHER INFORMATION: Contains the ICE-LAP-3 translational initiation site ATG
followed
344     by 5 nucleotides of ICE-LAP-3 coding sequence starting from the
345     initiation codon
347 <400> SEQUENCE: 9
348 gactatgcgt gcggggacac gg                                22
351 <210> SEQ ID NO: 10
352 <211> LENGTH: 53
353 <212> TYPE: DNA
354 <213> ORGANISM: Artificial sequence
356 <220> FEATURE:
357 <223> OTHER INFORMATION: Contains translation stop codon, HA tag and the last 21
358     nucleotides of the ICE-LAP-3 coding sequence, not including the
359     stop codon
361 <400> SEQUENCE: 10
362 aatcaagcgt agtctgggac gtcgtatggg tattcacctt ggtggaggat ttg            53
365 <210> SEQ ID NO: 11
366 <211> LENGTH: 21
367 <212> TYPE: DNA
368 <213> ORGANISM: Artificial sequence
370 <220> FEATURE:
371 <223> OTHER INFORMATION: Contains the ICE-LAP-4 translational initiation site, ATG,
372     followed by 15 nucleotides of ICE-LAP-4 coding sequence starting
373     from the initiation codon
375 <400> SEQUENCE: 11
376 accatggaga acactgaaaa c                                21
379 <210> SEQ ID NO: 12
380 <211> LENGTH: 53
381 <212> TYPE: DNA
382 <213> ORGANISM: Artificial sequence
384 <220> FEATURE:
385 <223> OTHER INFORMATION: Contains translation stop codon, HA tag and the last 21
386     nucleotides of the ICE-LAP-4 coding sequence, not including the
387     stop codon
389 <400> SEQUENCE: 12
390 aatcaagcgt agtctgggac gtcgtatggg tagtgataaa aatagagttc ttt            53
393 <210> SEQ ID NO: 13
394 <211> LENGTH: 503
395 <212> TYPE: PRT
396 <213> ORGANISM: Caenorhabditis elegans
398 <400> SEQUENCE: 13
400 Met Met Arg Gln Asp Arg Arg Ser Leu Leu Glu Arg Asn Ile Met Met
401 1           5           10           15
404 Phe Ser Ser His Leu Lys Val Asp Glu Ile Leu Glu Val Leu Ile Ala
405           20           25           30
408 Lys Gln Val Leu Asn Ser Asp Asn Gly Asp Met Ile Asn Ser Cys Gly
409           35           40           45
412 Thr Val Arg Glu Lys Arg Arg Glu Ile Val Lys Ala Val Gln Arg Arg
413           50           55           60

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**VERIFICATION SUMMARY**

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